

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.

Application Serial Number: 10/502, 083  
Source: PCT  
Date Processed by STIC: 5-5-05

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PCT

## RAW SEQUENCE LISTING

DATE: 05/05/2005

PATENT APPLICATION: US/10/502,083

TIME: 10:26:07

Input Set : A:\Final sequence list-12810-00046-US.txt

Output Set: N:\CRF4\05052005\J502083.raw

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3 <110> APPLICANT: Lerchl, Jens
4     Heinz, Ernst
5     Zank, Thorsten
7 <120> TITLE OF INVENTION: Novel elongase gene and method for producing polyunsaturated
8     fatty acids
10 <130> FILE REFERENCE: 53262-20077.00/12810-00046
12 <140> CURRENT APPLICATION NUMBER: US 10/502,083
13 <141> CURRENT FILING DATE: 2004-07-22
15 <150> PRIOR APPLICATION NUMBER: PCT/EP 03/00221
16 <151> PRIOR FILING DATE: 2003-01-13
18 <150> PRIOR APPLICATION NUMBER: DE 102 03 713.2
19 <151> PRIOR FILING DATE: 2002-01-30
21 <150> PRIOR APPLICATION NUMBER: DE 102 05 607.2
22 <151> PRIOR FILING DATE: 2002-02-11
24 <160> NUMBER OF SEQ ID NOS: 2
26 <170> SOFTWARE: PatentIn version 3.3
29 <210> SEQ ID NO: 1
30 <211> LENGTH: 1066
31 <212> TYPE: DNA
32 <213> ORGANISM: Phytophthora infestans
34 <220> FEATURE:
35 <221> NAME/KEY: CDS
36 <222> LOCATION: (52)..(888)
38 <400> SEQUENCE: 1
39 gaattcggca cgaggttcgc acgtccatcg tctactcacc aacaagaagt c atg tcg 57
40                                     Met Ser
41                                     1
43 act gag cta ctg cag agc tac tac gcg tgg gcc aac gcc acg gag gcc 105
44 Thr Glu Leu Leu Gln Ser Tyr Tyr Ala Trp Ala Asn Ala Thr Glu Ala
45         5                10                15
47 aag ctg ctg gac tgg gtc gac cct gag ggc ggc tgg aag gtg cat cct 153
48 Lys Leu Leu Asp Trp Val Asp Pro Glu Gly Gly Trp Lys Val His Pro
49     20                25                30
51 atg gca gac tac ccc cta gcc aac ttc tcc agc gtc tac gcc atc tgc 201
52 Met Ala Asp Tyr Pro Leu Ala Asn Phe Ser Ser Val Tyr Ala Ile Cys
53 35                40                45                50
55 gtc gga tac ttg ctc ttc gta atc ttc ggc acg gcc ctg atg aaa atg 249
56 Val Gly Tyr Leu Leu Phe Val Ile Phe Gly Thr Ala Leu Met Lys Met
57         55                60                65
59 gga gtc ccc gcc atc aag acc agt cca tta cag ttt gtg tac aac ccc 297
60 Gly Val Pro Ala Ile Lys Thr Ser Pro Leu Gln Phe Val Tyr Asn Pro
61         70                75                80
63 atc caa gtc att gcc tgc tct tat atg tgc gtg gag gcc gcc atc cag 345

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64 Ile Gln Val Ile Ala Cys Ser Tyr Met Cys Val Glu Ala Ala Ile Gln
65      85      90      95
67 gcc tac cgc aac ggc tac acc gcc gcc ccg tgc aac gcc ttt aag tcc 393
68 Ala Tyr Arg Asn Gly Tyr Thr Ala Ala Pro Cys Asn Ala Phe Lys Ser
69      100      105      110
71 gac gac ccc gtc atg ggc aac gtt ctg tac ctc ttc tat ctc tcc aag 441
72 Asp Asp Pro Val Met Gly Asn Val Leu Tyr Leu Phe Tyr Leu Ser Lys
73 115      120      125      130
75 atg ctc gac ctg tgc gac aca gtc ttc att atc cta gga aag aag tgg 489
76 Met Leu Asp Leu Cys Asp Thr Val Phe Ile Ile Leu Gly Lys Lys Trp
77      135      140      145
79 aaa cag ctt tcc atc ttg cac gtg tac cac cac ctt acc gtg ctt ttc 537
80 Lys Gln Leu Ser Ile Leu His Val Tyr His His Leu Thr Val Leu Phe
81      150      155      160
83 gtc tac tat gtg acg ttc cgc gcc gct cag gac ggg gac tca tat gct 585
84 Val Tyr Tyr Val Thr Phe Arg Ala Ala Gln Asp Gly Asp Ser Tyr Ala
85      165      170      175
87 acc atc gtg ctc aac ggc ttc gtg cac acc atc atg tac act tac tac 633
88 Thr Ile Val Leu Asn Gly Phe Val His Thr Ile Met Tyr Thr Tyr Tyr
89      180      185      190
91 ttc gtc agc gcc cac acg cgc aac att tgg tgg aag aag tac ctc acg 681
92 Phe Val Ser Ala His Thr Arg Asn Ile Trp Trp Lys Lys Tyr Leu Thr
93 195      200      205      210
95 cgc att cag ctt atc cag ttc gtg acc atg aac gtg cag ggc tac ctg 729
96 Arg Ile Gln Leu Ile Gln Phe Val Thr Met Asn Val Gln Gly Tyr Leu
97      215      220      225
99 acc tac tct cga cag tgc cca ggc atg cct cct aag gtg ccg ctc atg 777
100 Thr Tyr Ser Arg Gln Cys Pro Gly Met Pro Pro Lys Val Pro Leu Met
101      230      235      240
103 tac ctt gtg tac gtg cag tca ctc ttc tgg ctc ttc atg aat ttc tac 825
104 Tyr Leu Val Tyr Val Gln Ser Leu Phe Trp Leu Phe Met Asn Phe Tyr
105      245      250      255
107 att cgc gcg tac gtg ttc ggc ccc aag aaa ccg gcc gtg gag gaa tcg 873
108 Ile Arg Ala Tyr Val Phe Gly Pro Lys Lys Pro Ala Val Glu Glu Ser
109      260      265      270
111 aag aag aag ttg taa cggcgcttgt taaaaagtct aacctcgctg taacagctta 928
112 Lys Lys Lys Leu
113 275
115 aaacacacac acacacaacg cttttagtagag gaggtaagta gtggcaactc gtgtagaaat 988
117 gcagcatgcc catcaaatat atcccgtagt attcaaaaaa aaaaaaaaaa aaaaaaaaaa 1048
119 aaaaaaaaaa aactcgag 1066
122 <210> SEQ ID NO: 2
123 <211> LENGTH: 278
124 <212> TYPE: PRT
125 <213> ORGANISM: Phytophthora infestans
127 <400> SEQUENCE: 2
128 Met Ser Thr Glu Leu Leu Gln Ser Tyr Tyr Ala Trp Ala Asn Ala Thr
129 1 5 10 15
131 Glu Ala Lys Leu Leu Asp Trp Val Asp Pro Glu Gly Gly Trp Lys Val

```

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```

132          20          25          30
134 His Pro Met Ala Asp Tyr Pro Leu Ala Asn Phe Ser Ser Val Tyr Ala
135          35          40          45
137 Ile Cys Val Gly Tyr Leu Leu Phe Val Ile Phe Gly Thr Ala Leu Met
138          50          55          60
140 Lys Met Gly Val Pro Ala Ile Lys Thr Ser Pro Leu Gln Phe Val Tyr
141 65          70          75          80
143 Asn Pro Ile Gln Val Ile Ala Cys Ser Tyr Met Cys Val Glu Ala Ala
144          85          90          95
146 Ile Gln Ala Tyr Arg Asn Gly Tyr Thr Ala Ala Pro Cys Asn Ala Phe
147          100         105         110
149 Lys Ser Asp Asp Pro Val Met Gly Asn Val Leu Tyr Leu Phe Tyr Leu
150          115         120         125
152 Ser Lys Met Leu Asp Leu Cys Asp Thr Val Phe Ile Ile Leu Gly Lys
153          130         135         140
155 Lys Trp Lys Gln Leu Ser Ile Leu His Val Tyr His His Leu Thr Val
156 145          150         155         160
158 Leu Phe Val Tyr Tyr Val Thr Phe Arg Ala Ala Gln Asp Gly Asp Ser
159          165         170         175
161 Tyr Ala Thr Ile Val Leu Asn Gly Phe Val His Thr Ile Met Tyr Thr
162          180         185         190
164 Tyr Tyr Phe Val Ser Ala His Thr Arg Asn Ile Trp Trp Lys Lys Tyr
165          195         200         205
167 Leu Thr Arg Ile Gln Leu Ile Gln Phe Val Thr Met Asn Val Gln Gly
168          210         215         220
170 Tyr Leu Thr Tyr Ser Arg Gln Cys Pro Gly Met Pro Pro Lys Val Pro
171 225          230         235         240
173 Leu Met Tyr Leu Val Tyr Val Gln Ser Leu Phe Trp Leu Phe Met Asn
174          245         250         255
176 Phe Tyr Ile Arg Ala Tyr Val Phe Gly Pro Lys Lys Pro Ala Val Glu
177          260         265         270
179 Glu Ser Lys Lys Lys Leu
180          275

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**RAW SEQUENCE LISTING ERROR SUMMARY**  
PATENT APPLICATION: US/10/502,083

DATE: 05/05/2005  
TIME: 10:26:08

Input Set : A:\Final sequence list-12810-00046-US.txt  
Output Set: N:\CRF4\05052005\J502083.raw

**Invalid Line Length:**

The rules require that a line not exceed 72 characters in length. This includes spaces.

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Seq#:1; Line(s) 49,50,51,52,53,54,55,56,57,58,59,60,61,62,63,64,65,66,67,68  
Seq#:1; Line(s) 69,70,71,72,73,74,75,76,77,78,79,80,81,82,83,84,85,86,87,88  
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Seq#:2; Line(s) 138,139,140,141,142,143,144,145,146,147,148,149,150,151,152  
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Seq#:2; Line(s) 168,169,170,171,172,173,174,175,176,177,178,179

**VERIFICATION SUMMARY**

DATE: 05/05/2005

PATENT APPLICATION: US/10/502,083

TIME: 10:26:08

Input Set : A:\Final sequence list-12810-00046-US.txt

Output Set: N:\CRF4\05052005\J502083.raw